



#5

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/979,558

Source: Pt/09

Date Processed by STIC: 12/4/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

**ERROR DETECTED**

**SUGGESTED CORRECTION**

SERIAL NUMBER: 09/979,558

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
     (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
     <210> sequence id number  
     <400> sequence id number  
     000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/979,558

DATE: 12/04/2001

TIME: 11:49:56

Input Set : A:\PH-999PCT-USseq.txt

Output Set: N:\CRF3\11212001\I979558.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Secretary of Agency of Industrial Science and Technology  
 5 <120> TITLE OF INVENTION: Novel Psychrotrophic Bacteria and DNA Probes for Detecting  
 6 The Bacteria  
 8 <130> FILE REFERENCE: PH-999-PCT  
 OK 10 <140> CURRENT APPLICATION NUMBER: US/09/979,558  
 10 <141> CURRENT FILING DATE: 2001-11-23  
 10 <150> PRIOR APPLICATION NUMBER: JP 11-145342  
 11 <151> PRIOR FILING DATE: 1999-05-25  
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP00/02045  
 14 <151> PRIOR FILING DATE: 2000-03-30  
 16 <160> NUMBER OF SEQ ID NOS: 10  
 18 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

145 <210> SEQ ID NO: 10  
 146 <211> LENGTH: 18  
 147 <212> TYPE: DNA  
 148 <213> ORGANISM: Artificial Sequence  
 150 <220> FEATURE:  
 151 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
 153 <400> SEQUENCE: 10  
 154 gacgggcggt gtgtacaa 18  
 E--> 157 3/6 delete

see next page for more errors

<210> 1  
 <211> 1526  
 <212> DNA  
 <213> Psychrobacter pacificensis

<220>  
 <221> rRNA  
 <222> (1)..(1526)

<400> 1  
 tttgatcatg gctccagatt gaacgactgg gcggcaggct taacacatgc aagtcgagcg 60  
 gaaacgatga tagcttgcta ttaggcgtcg agcggccgga cgggtgagta atacttagga 120  
 atctacctag tagtggggga tagctcgggg aaactcgaat taataccgca tacgtctacg 180  
 ggagaaagca gggggtcatt agaccttgcg ctattagatg agcctaagtc ggattagcta 240  
 gatggtgggg taaaggccta ccatggcgac gatctgtagc tggctctgaga ggatgatcag 300  
 ccacaccggg actgagacac ggcccggact ctacgggagg cagcagtggg gaatattgga 360  
 caatgggggg aaccctgac cagccatgcc gcgtgtgtga agaaggcctt ttggttgtaa 420  
 agcactttaa gcagtgaaga agactcttcg gtttaataccc ggggacgatg acattagctg 480  
 cagaataagc accggctaac tctgtgccag cagccgcggt aatacagagg gtgcaagcgt 540  
 taatcggaat tactgggcgt aaagcgagcg taggtggcct gataagtcag atgtgaaatc 600  
 cccgggctta acctgggaac tgcattctgaa actgttaggc tagagtaggt gagagggaaag 660  
 tagaatttca ggtgtagcgg tgaaatgcgt agagatctga aggaataaccg atggcgaagg 720  
 cagcttcctg gcatcatact gacactgagg ctcgaaagcg tgggtagcaa acaggattag 780  
 ataccctggt agtccacgcc gtaaacgatg tctactagtc gttgggtccc ttgaggactt 840  
 agtgacgcag ctaacgcaat aagtagaccg cctggggagt acggccgcaa ggttaaaaact 900  
 caaatgaatt gacggggggc cgcacaagcg gtggagcatg tggtttaatt cgatgcaacg 960  
 cgaagaacct tacctggtct tgacatacac agaactctgt agagatacga gagtgccttc 1020  
 gggaattgtg atacagggtc tgcattggctc tcgtcagctc gtgtcgtgag atgttggggt 1080  
 aagtcccgca acgagcgcaa cccttgtcct tagttaccag cacttcgggt gggaactota 1140  
 aggatactgc cagtgacaaa ctggaggaag gcggggacga cgtcaagtca tcatggccct 1200  
 tacgaccagg gctacacacg tgctacaatg gtaggtacag agggcagcta cacagcgatg 1260  
 tgatgcgaat ctcaaaaagc ctatcgtagt ccagattgga gtctgcaact cgactccatg 1320  
 aagtaggaat cgctagtaat cgcggatcag aatgccgcgg tgaatacgtt cccgggcctt 1380  
 gtacacaccg cccgtcacac catgggagtt gattgcacca gaagtgggta gcctaactta 1440  
 gtgagggcga tcaccacggt gtggtcgatg actggggtga agtcgtaaca aggtagccgt 1500  
 aggggaacct gcggctggat cacctc 1526

see  
 item 9  
 on  
 Error  
 Summary  
 sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/979,558

DATE: 12/04/2001

TIME: 11:49:57

Input Set : A:\PH-999PCT-USseq.txt

Output Set: N:\CRF3\11212001\I979558.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:31 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:31 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:33 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:36 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:157 M:254 E: No. of Bases conflict, LENGTH:Input:6 Counted:19 SEQ:10  
L:157 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:157 M:252 E: No. of Seq. differs, <211>LENGTH:Input:18 Found:19 SEQ:10